

AMP2.txt  
SEQUENCE LISTING

<110> Liu, Chuan-Fa  
Feige, Ulrich  
Cheetham, Janet C.

<120> Thrombopoietic Compounds

<130> 01017/36263

<140>  
<141>

<150> 60/105,348  
<151> 1998-10-23

<160> 46

<170> PatentIn Ver. 2.0

<210> 1  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 1  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
1 5 10

<210> 2  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<223> Peptide is a subunit of a homodimer: Subunits in  
the dimer are covalently bonded at each carboxy  
terminus through peptide linkage with  
NH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-CH<sub>2</sub>-CH(COHNH)-NH-CO-CH<sub>2</sub>-CH<sub>2</sub>-NH<sub>2</sub>

<400> 2  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
1 5 10

<210> 3  
<211> 684  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 3  
atggacaaaa ctcacacatg tccacacctgt ccagctccgg aactcctggg gggaccgtca 60  
gtcttccctct tccccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc 120  
acatgcgtgg tggtgacgt gagccacgaa gaccctgagg tcaagttcaa ctggtagtgc 180  
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacacgcacg 240  
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggaggtac 300

## AMP2.txt

aagtgcagg	tctccaacaa	agccctccca	gccccatcg	agaaaaccat	ctccaaagcc	360
aaaggggcgc	cccggagaacc	acaggtgtac	accctgcccc	catcccggga	tgagctgacc	420
aagaaccagg	tcagcctgac	ctgcctggtc	aaaggctct	atcccagcga	catcgccgtg	480
gagtgggaga	gcaatgggca	gcccggagaac	aactacaaga	ccacgcctcc	cgtgctggac	540
tccgacggct	ctttcttcct	ctacagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	600
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	660
agcctctccc	tgtctccggg	taaa				684

&lt;210&gt; 4

&lt;211&gt; 684

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:  
oligonucleotide

&lt;400&gt; 4

tacctgtttt	gagtgtgtac	agggtggaca	ggtcgaggcc	ttgaggaccc	ccctggcagt	60
cagaaggaga	aggggggttt	tgggttcctg	tgggagact	agagggcctg	gggactccag	120
tgtacgcacc	accacctgca	ctcgggtgctt	ctgggactcc	agttcaagtt	gaccatgcac	180
ctgcccacc	tccacgtatt	acggttctgt	ttcgggcgcc	tccctgtcat	gttgtcgtgc	240
atggcacacc	agtgcggagga	gtggcaggac	gtggtcctga	ccgacttacc	gttccctcatg	300
ttcacgttcc	agaggttgg	tcgggaggg	cggggttagc	tcttttggta	gaggttcgg	360
tttcccgtcg	gggccttgg	tgtccacatg	tgggacgggg	gtagggccct	actcgactgg	420
ttcttggtcc	agtccgactg	gacggaccag	tttccgaaga	tagggtcgct	gtacggcac	480
ctcacccctct	cggttaccctgt	cggcctcttg	ttgatgttct	gttgccggagg	gcacgacactg	540
aggctgcccga	ggaagaagga	gatgtcggtc	gagtggcacc	tgttctcgct	caccgtcg	600
cccttgcaga	agagtacgag	gcactacgta	ctccgagacg	tgttggtat	gtgcgtcttc	660
tcggagaggg	acagaggccc	attt				684

&lt;210&gt; 5

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: peptide

&lt;400&gt; 5

Met	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
1							5		10				15		

Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
								25					30		

Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
								35				45			

His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
						50		55			60				

Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
						65		70		75		80			

Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
							85		90			95			

Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
							100		105			110			

Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
							115		120			125			

Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
						130		135			140				

AMP2.txt

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
210 215 220

Ser Pro Gly Lys  
225

<210> 6

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 6

Gly Gly Gly Lys Gly Gly Gly  
1 5

<210> 7

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 7

Gly Gly Gly Asn Gly Ser Gly Gly  
1 5

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 8

Gly Gly Gly Cys Gly Gly Gly  
1 5

<210> 9

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 9

Gly Pro Asn Gly  
1

<210> 10  
<211> 32  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 10  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Pro  
1 5 10 15  
Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
20 25 30

<210> 11  
<211> 36  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<223> Cyclic peptide; Secondary structure is maintained  
by disulfide bond between intramolecular Cys  
residues at positions 9 and 31

<400> 11  
Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 12  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 12  
Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Arg Leu Gln Cys Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 13

AMP2.txt

<211> 36  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: peptide  
  
<400> 13  
Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 14  
<211> 36  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: peptide  
  
<400> 14  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Lys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 15  
<211> 36  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Lys residue at position 18 is Bromoacetylated  
  
<220>  
<223> Description of Artificial Sequence: derivatized  
peptide  
  
<400> 15  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Lys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 16  
<211> 36  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: peptide

AMP2.txt

<400> 16  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Cys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 17  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Lys at position 18 is pegylated

<220>  
<223> Description of Artificial Sequence: derivatized peptide

<400> 17  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Lys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 18  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Cys at position 18 is pegylated

<220>  
<223> Description of Artificial Sequence: derivatized peptide

<400> 18  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Cys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 19  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 19

AMP2.txt

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Asn Gly Ser Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 20  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Monomeric subunit of a homodimer; Subunits in the  
homodimer are bonded by a disulfide bond between  
Cys residues at position 18 on each subunit

<220>  
<223> Description of Artificial Sequence: peptide

<400> 20  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Cys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 21  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 21  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 22  
<211> 32  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Peptide is derivatized at the amino terminus with a  
covalently bonded immunoglobulin Fc region

<220>  
<223> Description of Artificial Sequence: peptide

<400> 22  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Pro  
Page 7

Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
20 25 30

<210> 23

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide is covalently bonded at the amino and carboxy termini to an immunoglobulin Fc region

<220>

<223> Description of Artificial Sequence: peptide

<400> 23

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Pro  
1 5 10 15

Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
20 25 30

<210> 24

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide is copvalently bonded at the carboxy terminus to an immunoglobulin Fc region

<220>

<223> Description of Artificial Sequence: peptide

<400> 24

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30

Ala Ala Arg Ala  
35

<210> 25

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide is covalently bonded at the amino terminus to an immunoglobulin Fc region

<220>

<223> Description of Artificial Sequence: peptide

AMP2.txt

<400> 25  
Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
1 5 10 15  
Gly Pro Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala  
20 25 30  
Arg Ala

<210> 26  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Peptide is covalently bonded at the amino terminus  
to an immunoglobulin Fc region

<220>  
<223> Description of Artificial Sequence: peptide

<400> 26  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 27  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Peptide is covalently bonded at the amino terminus  
to an immunoglobulin Fc region

<220>  
<223> Cyclic peptide; Secondary structure is maintained  
by disulfide linkage between intramolecular Cys  
residues at positions 9 and 31

<220>  
<223> Description of Artificial Sequence: peptide

<400> 27  
Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 28  
<211> 36  
<212> PRT  
<213> Artificial Sequence

AMP2.txt

<220>  
<223> Peptide is covalently bonded at the amino terminus  
to an immunoglobulin Fc region

<220>  
<223> Description of Artificial Sequence: peptide

<400> 28  
Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 29  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<223> Peptide is covalently bonded at the amino terminus  
to an immunoglobulin Fc region

<400> 29  
Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 30  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Peptide is covalently bonded at the amino terminus  
to an immunoglobulin Fc region

<220>  
<223> Description of Artificial Sequence: peptide

<400> 30  
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15  
Gly Lys Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30  
Ala Ala Arg Ala  
35

<210> 31  
<211> 36  
<212> PRT

AMP2.txt

<213> Artificial Sequence

<220>

<223> Peptide is covalently bonded at the amino terminus  
to an immunoglobulin Fc region

<220>

<223> Description of Artificial Sequence: peptide

<400> 31

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Cys Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30

Ala Ala Arg Ala  
35

<210> 32

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<223> Peptide is covalently bonded at the amino terminus  
to an immunoglobulin Fc region

<400> 32

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Asn Gly Ser Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30

Ala Ala Arg Ala  
35

<210> 33

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<223> Peptide is a subunit of a homodimer; Subunits in  
the homodimer are covalently bonded through a  
disulfide bond between Cys residues at position 18  
of each subunit

<220>

<223> Peptide is covalently bonded at the amino terminus  
to an immunoglobulin Fc region

<400> 33

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Cys Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30

AMP2.txt

Ala Ala Arg Ala  
35

<210> 34  
<211> 41  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<223> Peptide is covalently bonded at the amino terminus  
to an immunoglobulin Fc region

<400> 34  
Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala  
1 5 10 15  
Ala Arg Ala Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr  
20 25 30  
Leu Arg Gln Trp Leu Ala Ala Arg Ala  
35 40

<210> 35  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 35  
aaaggtggag gtgggtggat cgaagggtccg actctgcgtc agtggctggc tgctcggt 60

<210> 36  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 36  
acctccacca ccagcacgag cagccagcca ctgacgcaga gtcggacc 48

<210> 37  
<211> 66  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 37  
ggtgtggag gtggcggcgg aggtatttag ggcccaaccc ttcgccaatg gcttgcagca 60  
66  
cgcgca

<210> 38  
<211> 76

AMP2.txt

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 38  
aaaaaaaaagga tcctcgagat tatgcgcgtg ctgcaagcca ttggcgaagg gttggccct 60  
caataacctcc gccgcc 76

<210> 39  
<211> 126  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 39  
aaagggtggag gtgggttat cgaagggtccg actctgcgtc agtggctggc tgctcgtgct 60  
ggtgtggag gtggcggcgg aggtatttag ggcaccaacc ttcgcataatg gcttgcagca 120  
cgcgca 126

<210> 40  
<211> 124  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 40  
ccaggttgag acgcgtcac cgaccgacga gcacgaccac cacctccacc gcccctcca 60  
taactcccg gttggaaagc gtttaccgaa cgtcgtgcgc gtattagagc tccttagaaaa 120  
aaaa 124

<210> 41  
<211> 42  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 41  
Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
1 5 10 15

Ala Ala Arg Ala Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro  
20 25 30

Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
35 40

<210> 42  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

## AMP2.txt

<400> 42  
aacataagta cctgtaggat cg

22

<210> 43  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 43  
ttcgatacca ccacacctcac ctttacccgg agacagggag aggctttct gc 52

<210> 44  
<211> 861  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 44  
tcttagattt ttttaactaa tttaaggagg aataacatat ggacaaaact cacacatgtc 60  
caccttgtcc agctccggaa ctctggggg gaccgtcagt cttcctttc ccccaaaaac 120  
ccaaggacac cctcatgatc tcccgaccc ctgaggtcac atgcgtgggt gtggacgtga 180  
gccacgaaga ccctgagggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 240  
ccaagacaaa gccgcggggag gaggcgtaca acagcacgtc ccgtgtggtc agcgtccctca 300  
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc tccaacaaaag 360  
ccctccccagc ccccatcgag aaaaccatct ccaaaggccaa agggcagccc cgagaaccac 420  
aggtgtacac cctgccccca tcccggtatg agctgaccaa gaaccagggtc agcctgaccc 480  
gcctggtaa aggcttctat cccagcgaca tcgcccgtgga gtggggagagc aatgggcagc 540  
cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggcttc ttcttcctct 600  
acagcaagct caccgtgac aagagcagggt ggcagcagggt gaacgtttc tcattgtccg 660  
tgatgtatca ggctctgtac aaccactaca cgcagaagag ccttccctgt tctccggta 720  
aagggtgggg tgggtgtatc aaagggtccga ctctcgatca gtggctgggt gctcgctgt 780  
gtgggtgggg tggcggccgaa ggtattgagg gcccaaccct tcgccaatgg ctgcagcac 840  
gcgcataatc tcgaggatcc g 861

<210> 45  
<211> 861  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 45  
agatctaaac aaaattgatt aatttcctcc ttattgtata cctgtttga gtgtgtacag 60  
gtgaaacagg tcgaggcctt gaggacccc ctggcagtca gaaggagaag gggggttttg 120  
ggttctgtg ggagtagtag agggcctggg gactccagtg tagcaccac caccgtcact 180  
cggtgtttct gggactccag ttcaagttga ccatgacccct ggcgcaccc cacgtattac 240  
ggttctgtt cggcgcctct ctcgtcatgt tgcgtgcacat ggcacaccag tcgcaggagt 300  
ggcaggacgt ggtcctgacc gacttaccgt tcctcatgtt cacgtccag aggtttttc 360  
gggggggtcg ggggttagtc tttttgtaga ggtttcggtt tcccgtcggg gctttgggt 420  
tccacatgtg ggacgggggt agggccctac tcgactgggt ttggccatc tcggactgg 480  
cggaaggatc tccgaagata gggtcgtgt agcggcacct caccctctcg ttaccgtcg 540  
gcctttgtt gatgttctgg tgcggagggc acgaccgttag gtcggcagg aagaaggaga 600  
tgtcggtcgat gttggcacctg ttctcgatca ccgtcgatccc ttgcagaag agtacgaggc 660  
actacgtact ccgagacgtg ttgggtatgt gcgtttctc ggagagggac agaggccat 720  
ttccacactcc accaccatag ctccaggct gagacgcagt caccgaccga cgagcacgac 780  
caccacactcc accgcccgcct ccataactcc cgggttggga agcggttacc gaacgtcgat 840  
cgcgatccatc agtcctttagg c 861

AMP2.txt

<210> 46  
<211> 269  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 46  
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
1 5 10 15  
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
20 25 30  
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
35 40 45  
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
50 55 60  
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
65 70 75 80  
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
85 90 95  
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
100 105 110  
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125  
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
130 135 140  
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160  
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175  
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190  
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
195 200 205  
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
210 215 220  
Ser Pro Gly Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg  
225 230 235 240  
Gln Trp Leu Ala Ala Arg Ala Gly Gly Gly Gly Gly Gly Ile  
245 250 255  
Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
260 265